

## **RAW SEQUENCE LISTING**

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Application Serial Number: 10/659,755B  
Source: JFW/6  
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IFW16

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DATE: 04/09/2007

PATENT APPLICATION: US/10/659,755B

TIME: 15:00:08

Input Set : N:\EFS\04\_09\_07\10659755B\_efs\NBLE007US.txt

Output Set: N:\CRF4\04092007\J659755B.raw

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3 <110> APPLICANT: DIXON, RICHARD A.
4     LIU, CHANG-JUN
5     DEAVOURS, BETTINA
7 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCTION OF FLAVONOID
8     AND ISOFLAVONOID NUTRACEUTICALS
10 <130> FILE REFERENCE: NBLE:007US
12 <140> CURRENT APPLICATION NUMBER: 10/659,755B
13 <141> CURRENT FILING DATE: 2003-09-10
15 <150> PRIOR APPLICATION NUMBER: 60/409,447
16 <151> PRIOR FILING DATE: 2002-09-10
18 <160> NUMBER OF SEQ ID NOS: 15
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1824
24 <212> TYPE: DNA
25 <213> ORGANISM: Soybean
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29 ttgaacttgc acttggttta ttggttttgg ctctgtttct gcacttgcg cccacaccca 120
30 ctgcaaaatc aaaagcactt cgccatctcc caaaccacc aagcccaaag cctcgtcttc 180
31 cttcatagg acaccttcat ctcttaaaag acaaacttct ccactacgca ctcatcgacc 240
32 tctccaaaaa acatgggtccc ttattctctc tctactttgg ctccatgcca accgttggtg 300
33 cctccacacc agaattgttc aagctcttcc tccaaacgca cgaggcaact tccttcaaca 360
34 caaggttcca aacctcagcc ataagacgcc tcacctatga tagctcagt gccatgggtc 420
35 cttcgggacc ttactggaag ttcgtgagga agctcatcat gaacgacctt cccaacgcca 480
36 ccactgtaaa caagttgagg cttttgagga cccaacagac ccgcaagttc cttagggtta 540
37 tggcccaagg cgcagaggca cagaagcccc ttgacttgac cgaggagctt ctgaaatgga 600
38 ccaacagcac catctccatg atgatgctcg gcgaggctga ggagatcaga gacatcgctc 660
39 gcgaggttct taagatcttt ggcgaataca gcctcactga cttcatctgg ccattgaagc 720
40 atctcaaggt tggaaagtat gagaagagga tgcagacat cttgaacaag ttcgacctg 780
41 tcgttgaaag ggtcatcaag aagcgccgtg agatcgtag gaggagaaag aacggagagg 840
42 ttgttgaggg tgaggtcagc ggggttttcc ttgacacttt gcttgaattc gctgaggatg 900
43 agaccatgga gatcaaaatc accaaggacc acatcgaggg tcttgttggt gactttttct 960
44 cggcaggaac agactccaca gcggtggcaa cagagtgggc attggcagaa ctcatcaaca 1020
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48 atggatatgt gatcccagag ggagcattga ttctcttcaa tgtatggcaa gtaggaagag 1260
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52 ttgcatctct tattcagtgc ttgcacttgc aagtgtggg tccacaagga cagatattga 1500
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54 atagtcttgt ctgtgttcca cttgcaagga tcggcggtgc atctaaactc ctttcttaat 1620
55 taagatcatc atcatatata atatttactt tttgtgtgtt gataatcatc atttcaataa 1680
56 ggtctcgttc atctactttt tatgaagtat ataagccctt ccatgcacat tgtatcatct 1740
57 cccatttgtc ttcgtttgtc acctaaggca atcttttttt ttttagaatc acatcatcct 1800
58 actataaact atcaatcctt atat                                     1824
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62 <211> LENGTH: 521
63 <212> TYPE: PRT
64 <213> ORGANISM: Soybean
66 <400> SEQUENCE: 2
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68 1 5 10 15
70 His Leu Arg Pro Thr Pro Thr Ala Lys Ser Lys Ala Leu Arg His Leu
71 20 25 30
73 Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly His Leu
74 35 40 45
76 His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp Leu Ser
77 50 55 60
79 Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met Pro Thr
80 65 70 75 80
82 Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr His
83 85 90 95
85 Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg
86 100 105 110
88 Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Phe Gly Pro Tyr Trp
89 115 120 125
91 Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Pro Asn Ala Thr Thr
92 130 135 140
94 Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Thr Arg Lys Phe Leu
95 145 150 155 160
97 Arg Val Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp Leu Thr
98 165 170 175
100 Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met Met Leu
101 180 185 190
103 Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu Lys Ile
104 195 200 205
106 Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys His Leu
107 210 215 220
109 Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn Lys Phe
110 225 230 235 240
112 Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile Val Arg
113 245 250 255
115 Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Val Ser Gly Val Phe
116 260 265 270
118 Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu Ile Lys
119 275 280 285
121 Ile Thr Lys Asp His Ile Glu Gly Leu Val Val Asp Phe Phe Ser Ala
122 290 295 300
124 Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala Glu Leu

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127 Ile Asn Asn Pro Lys Val Leu Glu Lys Ala Arg Glu Glu Val Tyr Ser
128          325          330          335
130 Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln Asn Leu
131          340          345          350
133 Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His Pro Pro
134          355          360          365
136 Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile Asn Gly
137          370          375          380
139 Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn Val Trp Gln Val
140 385          390          395          400
142 Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg Pro Glu
143          405          410          415
145 Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Gly Pro Leu Asp Leu
146          420          425          430
148 Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg Met
149          435          440          445
151 Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu Leu Ala
152          450          455          460
154 Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln Gly Gln
155 465          470          475          480
157 Ile Leu Lys Gly Gly Asp Ala Lys Val Ser Met Glu Glu Arg Ala Gly
158          485          490          495
160 Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu Ala Arg
161          500          505          510
163 Ile Gly Val Ala Ser Lys Leu Leu Ser
164          515          520
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168 <211> LENGTH: 950
169 <212> TYPE: DNA
170 <213> ORGANISM: Medicago sativa
172 <220> FEATURE:
173 <221> NAME/KEY: CDS
174 <222> LOCATION: (41)..(709)
176 <400> SEQUENCE: 3
177 gaattcccat agctaaacaa aaaaaattaa gaacaagaat atg gct gca tca atc 55
178          Met Ala Ala Ser Ile
179          1          5
181 acc gca atc act gtg gag aac ctt gaa tac cca gcg gtg gtt acc tct 103
182 Thr Ala Ile Thr Val Glu Asn Leu Glu Tyr Pro Ala Val Val Thr Ser
183          10          15          20
185 ccg gtc acc ggc aaa tca tat ttc ctc ggt ggc gct ggg gag aga gga 151
186 Pro Val Thr Gly Lys Ser Tyr Phe Leu Gly Gly Ala Gly Glu Arg Gly
187          25          30          35
189 ttg acc att gaa gga aac ttc atc aag ttc act gcc ata ggt gtt tat 199
190 Leu Thr Ile Glu Gly Asn Phe Ile Lys Phe Thr Ala Ile Gly Val Tyr
191          40          45          50
193 ttg gaa gat ata gca gtg gct tca cta gct gcc aaa tgg aag ggt aaa 247
194 Leu Glu Asp Ile Ala Val Ala Ser Leu Ala Ala Lys Trp Lys Gly Lys

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195      55      60      65
197 tca tct gaa gag tta ctt gag acc ctt gac ttt tac aga gac atc atc 295
198 Ser Ser Glu Glu Leu Leu Glu Thr Leu Asp Phe Tyr Arg Asp Ile Ile
199 70      75      80      85
201 tca ggt ccc ttt gaa aag tta att aga ggg tca aag att agg gaa ttg 343
202 Ser Gly Pro Phe Glu Lys Leu Ile Arg Gly Ser Lys Ile Arg Glu Leu
203      90      95      100
205 agt ggt cct gag tac tca agg aag gtt atg gag aac tgt gtg gca cac 391
206 Ser Gly Pro Glu Tyr Ser Arg Lys Val Met Glu Asn Cys Val Ala His
207      105      110      115
209 ttg aaa tca gtt gga act tat gga gat gca gaa gct gaa gct atg caa 439
210 Leu Lys Ser Val Gly Thr Tyr Gly Asp Ala Glu Ala Glu Ala Met Gln
211      120      125      130
213 aaa ttt gct gaa gct ttc aag cct gtt aat ttt cca cct ggt gcc tct 487
214 Lys Phe Ala Glu Ala Phe Lys Pro Val Asn Phe Pro Pro Gly Ala Ser
215      135      140      145
217 gtt ttc tac agg caa tca cct gat gga ata tta ggg ctt agt ttc tct 535
218 Val Phe Tyr Arg Gln Ser Pro Asp Gly Ile Leu Gly Leu Ser Phe Ser
219 150      155      160      165
221 ccg gat aca agt ata cca gaa aag gag gct gca ctc ata gag aac aag 583
222 Pro Asp Thr Ser Ile Pro Glu Lys Glu Ala Ala Leu Ile Glu Asn Lys
223      170      175      180
225 gca gtt tca tca gca gtg ttg gag act atg atc ggc gag cac gct gtt 631
226 Ala Val Ser Ser Ala Val Leu Glu Thr Met Ile Gly Glu His Ala Val
227      185      190      195
229 tcc cct gat ctt aag cgc tgt tta gct gca aga tta cct gcg ttg ttg 679
230 Ser Pro Asp Leu Lys Arg Cys Leu Ala Ala Arg Leu Pro Ala Leu Leu
231      200      205      210
233 aac gag ggt gct ttc aag att gga aac tga tgatgattat actcctatat 729
234 Asn Glu Gly Ala Phe Lys Ile Gly Asn
235      215      220
237 cactgcattt ccaaaagcgt tgcagcacaa gaatgagacc atgaactttt ttaagtctac 789
239 acgtttaatt ttttgtatat ctatttacct tcttattagt atcaataata tgaaatgaaa 849
241 gatcttgctt tctactcttg tactatttct gtgatagata atgttaatga gtatcttcat 909
243 caataaaaagt gatttgtttt gtttgttcaa aaaaaaaaaa a 950
246 <210> SEQ ID NO: 4
247 <211> LENGTH: 222
248 <212> TYPE: PRT
249 <213> ORGANISM: Medicago sativa
251 <400> SEQUENCE: 4
252 Met Ala Ala Ser Ile Thr Ala Ile Thr Val Glu Asn Leu Glu Tyr Pro
253 1      5      10      15
254 Ala Val Val Thr Ser Pro Val Thr Gly Lys Ser Tyr Phe Leu Gly Gly
255      20      25      30
256 Ala Gly Glu Arg Gly Leu Thr Ile Glu Gly Asn Phe Ile Lys Phe Thr
257      35      40      45
258 Ala Ile Gly Val Tyr Leu Glu Asp Ile Ala Val Ala Ser Leu Ala Ala
259      50      55      60
260 Lys Trp Lys Gly Lys Ser Ser Glu Glu Leu Leu Glu Thr Leu Asp Phe

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261 65              70              75              80
262 Tyr Arg Asp Ile Ile Ser Gly Pro Phe Glu Lys Leu Ile Arg Gly Ser
263              85              90              95
264 Lys Ile Arg Glu Leu Ser Gly Pro Glu Tyr Ser Arg Lys Val Met Glu
265              100             105             110
266 Asn Cys Val Ala His Leu Lys Ser Val Gly Thr Tyr Gly Asp Ala Glu
267              115             120             125
268 Ala Glu Ala Met Gln Lys Phe Ala Glu Ala Phe Lys Pro Val Asn Phe
269              130             135             140
270 Pro Pro Gly Ala Ser Val Phe Tyr Arg Gln Ser Pro Asp Gly Ile Leu
271 145             150             155             160
272 Gly Leu Ser Phe Ser Pro Asp Thr Ser Ile Pro Glu Lys Glu Ala Ala
273              165             170             175
274 Leu Ile Glu Asn Lys Ala Val Ser Ser Ala Val Leu Glu Thr Met Ile
275              180             185             190
276 Gly Glu His Ala Val Ser Pro Asp Leu Lys Arg Cys Leu Ala Ala Arg
277              195             200             205
278 Leu Pro Ala Leu Leu Asn Glu Gly Ala Phe Lys Ile Gly Asn
279              210             215             220
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284 <211> LENGTH: 836
285 <212> TYPE: DNA
286 <213> ORGANISM: Medicago sativa
288 <400> SEQUENCE: 5
289 caaatcatat ttcctcggtg gcgctgggga gagaggattg accattgaag gaaacttcat 60
290 caagttcact gccataggtg tttatttgga agatatagca gtggcttcac tagctgccaa 120
291 atggaagggt aaatcatctg aagagttact tgagaccctt gacttttaca gagacatcat 180
292 ctccaggtccc tttgaaaagt taattagagg gtcaaagatt agggaattga gtggtcctga 240
293 gtactcaagg aaggttatgg agaactgtgt ggcacacttg aaatcagttg gaacttatgg 300
294 agatgcagaa gctgaagcta tgcaaaaatt tgctgaagct ttcaagcctg ttaattttcc 360
295 acctggtgcc tctgttttct acaggcaatc acctgatgga atattagggc ttagttttctc 420
296 tccggataca agtataaccag aaaaggaggc tgcactcata gagaacaagg cagtttcac 480
297 agcagtgttg gagactatga tcggcgaaaca cgctgtttcc cctgatctta agcgtgtgtt 540
298 ggctgcaaga ttacctgcgt tgttgaacga ggggtgctttc aagattggaa actgatgatg 600
299 attatactct tatataaaaa catttccaaa agcgttgcag cacaagaatg agaccatgga 660
300 cttttttaag tctacacgtt taattttttg tatatctatt taccttctta ttagtatcaa 720
301 tagtatgaaa tgaaagatct tgctttctac tcttgtacta tttctgtgat agataatgtt 780
302 aatgagtatc ttcatacaata aaagtgatgtt gttttgtttg ttcaaaaaaa aaaaaa 836
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306 <211> LENGTH: 1380
307 <212> TYPE: DNA
308 <213> ORGANISM: Medicago sativa
310 <220> FEATURE:
311 <221> NAME/KEY: CDS
312 <222> LOCATION: (67)..(1236)
314 <400> SEQUENCE: 6
315 gaattcccaa caaacaagta ctgcaaacca attgagtatt acatagaaac tactagagat 60
317 accaag atg gtg agt gta tct gaa att cgc aag gct cag agg gca gaa 108
318 Met Val Ser Val Ser Glu Ile Arg Lys Ala Gln Arg Ala Glu

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VERIFICATION SUMMARY

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